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OM protein - protein search, using sw model

Run on: February 13, 2001, 19:46:08 ; Search time 59.97 Seconds
(without alignments)
656.693 Million cell updates/sec

Title: US-09-481-990-2
Perfect score: 1753
Sequence: 1 MLOSLAGSCVRLVERHRSR.....QNEPFAVQSSACVDGPANH 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_15:*
2: sp.archaea:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1753	100.0	336	4 000180	000180 homo sapien
2	1693	96.6	336	11 09822T2	09822T2 rattus norv
3	1658	94.6	336	11 008581	008581 mus musculu
4	1292.5	73.7	259	6 002821	002821 oryctolagus
5	653.5	37.3	313	4 09257	09257 homo sapien
6	532.5	30.4	343	11 093J14	093J14 mus musculu
7	521.5	29.7	307	4 09Y2U2	09Y2U2 homo sapien
8	518.5	29.6	307	11 09822T1	09822T1 mus musculu
9	430.5	24.6	392	5 09NEV3	09NEV3 caenorhabd1
10	396	22.6	538	11 09J1S4	09J1S4 rattus norv
11	381.5	21.8	426	4 095069	095069 homo sapien
12	379.5	21.6	411	11 088454	088454 mus musculu
13	379.5	21.6	411	4 09NRT2	09NRT2 homo sapien
14	378	21.6	419	4 09NYG8	09NYG8 homo sapien
15	376.5	21.5	411	11 097438	097438 mus musculu
16	369	20.5	502	11 09JK62	09JK62 mus musculu
17	359	20.5	499	4 095279	095279 homo sapien
18	333.5	19.0	299	11 09OX34	09OX34 mus musculu
19	333.5	19.0	409	11 035111	035111 mus musculu

20	333.5	19.0	411	11 054912	054912 rattus norv
21	321.5	18.3	395	11 09J1D4	09J1D4 rattus norv
22	320.5	18.3	394	4 014649	014649 homo sapien
23	316.5	18.1	374	4 09NPC2	09NPC2 homo sapien
24	310	17.7	365	11 09JL58	09JL58 cavia porce
25	303.5	17.3	385	5 09VYX5	09VYX5 drosophila
26	300	17.1	393	5 09XU07	09XU07 caenorhabd1
27	295	16.8	427	5 023386	023386 caenorhabd1
28	294.5	16.8	443	5 045422	045422 caenorhabd1
29	294	16.8	329	5 076790	076790 caenorhabd1
30	291	16.6	364	5 076790	076790 caenorhabd1
31	284.5	16.2	336	5 017185	017185 drosophila
32	278.5	15.9	340	5 09VHE0	09VHE0 drosophila
33	264.5	15.1	1001	5 094526	094526 drosophila
34	263	15.0	995	5 09W217	09W217 drosophila
35	256.5	14.6	475	5 023435	023435 caenorhabd1
36	251	14.3	383	5 021094	021094 caenorhabd1
37	251	14.3	398	5 09VFS9	09VFS9 drosophila
38	246	14.0	522	5 022042	022042 caenorhabd1
39	246	14.0	1910	5 022426	022426 caenorhabd1
40	245	14.0	395	5 09V362	09V362 drosophila
41	245	14.0	631	5 045894	045894 caenorhabd1
42	244	13.9	513	5 022940	022940 caenorhabd1
43	240	13.7	539	5 021505	021505 caenorhabd1
44	236	13.5	654	5 090863	090863 caenorhabd1
45	231	13.2	523	5 017935	017935 caenorhabd1

ALIGNMENTS

RESULT 1
ID 000180 PRELIMINARY; PRT; 336 AA.
AC 000180; Q13307;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1 (POTASSIUM CHANNEL KCNO1).
GN KCNK1 OR TWIK1 OR HOH01 OR KCNO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN 1
RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC MEDLINE=96183184; PubMed=8605869;
RA Lesage F., Guillemae E., Fink M., Duprat F., Lazdunski M., Romey G., Barhanin J.;
RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a novel structure.";
RL EMBO J. 15:1004-1011(1996).
RN 2
RP SEQUENCE FROM N.A., AND REVIEW.
RC TISSUE-BRAIN;
RA MEDLINE=98122696; PubMed=9462864;
RX Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
RT "Sequence and function of the two P domain potassium channels: implications of an emerging superfamily.";
RL J. Mol. Med. 76:13-20(1998).
RN 3
RP SEQUENCE FROM N.A.
RA Desit G.V., Orlas M., Freeman T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC 1- SUBUNIT: HOMODIMER (POTENTIAL).
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC 1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC - MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

CC EMBL: U33632; AAB01688.1; -;
 CC EMBL: U76996; AAB97878.1; -;
 DR EMBL: U90065; AAB51147.1; -;
 DR MIM: 601745; -;
 DR INTERPRO: IPR000099; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR001779; -;
 DR PFAM: PF02034; TWIK channel: 1.
 DR PRINTS: PR01096; TWIKCHANNEL.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 1 20
 FT TRANSMEM 21 41
 FT DOMAIN 104 130
 FT TRANSMEM 133 153
 FT DOMAIN 154 177
 FT TRANSMEM 178 198
 FT DOMAIN 212 238
 FT TRANSMEM 247 267
 FT DOMAIN 268 336
 FT MOD_RES 19
 FT MOD_RES 303
 FT CARBOHYD 95
 FT MUTAGEN 161
 SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

Query Match 100.0%; Score 1753; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.8e-135;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQSLAGSSCVLVERHRSAMCGFLVGLYLIVFGAVFSSVLPEDLLROELRLK 60
 DB 1 MQSLAGSSCVLVERHRSAMCGFLVGLYLIVFGAVFSSVLPEDLLROELRLK 60
 QY 61 RRFLEHEHCLSQOLEQFLGRVLEASNYGVSLSNAGSNMMDFTSALFFASTVLTGGY 120
 DB 61 RRFLEHEHCLSQOLEQFLGRVLEASNYGVSLSNAGSNMMDFTSALFFASTVLTGGY 120
 QY 121 GHTVPLSDGKAFCTIYVIGIPFLFLTAIVVORITVHVRPVLVYHIMGFSKOYVA 180
 DB 121 GHTVPLSDGKAFCTIYVIGIPFLFLTAIVVORITVHVRPVLVYHIMGFSKOYVA 180
 QY 181 IVHAVLLGFVTVSCFFETPAAVFSVLEDDMNFLESFYCFISLTIGLDVVPGEYNOK 240
 DB 181 IVHAVLLGFVTVSCFFETPAAVFSVLEDDMNFLESFYCFISLTIGLDVVPGEYNOK 240
 QY 241 FRELYKIGITCYLLGLTAMLVLETFCELHKKFRKMFYVKKDKDQVHIIEHDLS 300
 DB 241 FRELYKIGITCYLLGLTAMLVLETFCELHKKFRKMFYVKKDKDQVHIIEHDLS 300
 QY 301 FSSITDQAAGKEQKONEPVPATQSSACVDPANH 336
 DB 301 FSSITDQAAGKEQKONEPVPATQSSACVDPANH 336

RESULT 2
 092272 PRELIMINARY; PRT; 336 AA.
 AC 092272
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE POTASSIUM POTASSIUM CHANNEL TWIK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
 RA Kaczmarek L.K.;
 RT "Cloning and localization of rtwik, a putative potassium channel with
 RT two P domains";
 RL Submitted (Sep-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF022819; AAD09336.1; -;
 DR INTERPRO: IPR000099; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR001779; -;
 DR PFAM: PF02034; TWIK channel: 1.
 DR PRINTS: PR01096; TWIKCHANNEL.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR Ionic channel.
 KW SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 96.6%; Score 1693; DB 11; Length 336;
 Best Local Similarity 96.4%; Pred. No. 2.9e-130;
 Matches 324; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MQSLAGSSCVLVERHRSAMCGFLVGLYLIVFGAVFSSVLPEDLLROELRLK 60
 DB 1 MQSLAGSSCVLVERHRSAMCGFLVGLYLIVFGAVFSSVLPEDLLROELRLK 60
 QY 61 RRFLEHEHCLSQOLEQFLGRVLEASNYGVSLSNAGSNMMDFTSALFFASTVLTGGY 120
 DB 61 RRFLEHEHCLSQOLEQFLGRVLEASNYGVSLSNAGSNMMDFTSALFFASTVLTGGY 120
 QY 121 GHTVPLSDGKAFCTIYVIGIPFLFLTAIVVORITVHVRPVLVYHIMGFSKOYVA 180
 DB 121 GHTVPLSDGKAFCTIYVIGIPFLFLTAIVVORITVHVRPVLVYHIMGFSKOYVA 180
 QY 181 IVHAVLLGFVTVSCFFETPAAVFSVLEDDMNFLESFYCFISLTIGLDVVPGEYNOK 240
 DB 181 IVHAVLLGFVTVSCFFETPAAVFSVLEDDMNFLESFYCFISLTIGLDVVPGEYNOK 240
 QY 241 FRELYKIGITCYLLGLTAMLVLETFCELHKKFRKMFYVKKDKDQVHIIEHDLS 300
 DB 241 FRELYKIGITCYLLGLTAMLVLETFCELHKKFRKMFYVKKDKDQVHIIEHDLS 300
 QY 301 FSSITDQAAGKEQKONEPVPATQSSACVDPANH 336
 DB 301 FSSITDQAAGKEQKONEPVPATQSSACVDPANH 336

RESULT 3
 008581 PRELIMINARY; PRT; 336 AA.
 AC 008581
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1.
 GN KCNK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-BRAIN;
 RC MEDLINE=97165959; PubMed=9013852;
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
 RA Lazdunski M.;
 RT "The structure, function and distribution of the mouse TWIK-1 K+
 RT channel";
 RL FEBS Lett. 402:28-32(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=129/SVJ; TISSUE=LIVER;
 RC MEDLINE=98218573; PubMed=9559671;
 RX Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barbanin J.;

RT "Structure, chromosome localization, and tissue distribution of the
RT mouse twik k+ channel gene.";
RL FEBS Lett. 425:310-316(1998).
CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC CORTEX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC STABILIZES AFTER DAY 8.
CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC EMBL: AF033017; AAC16973.1; -.
CC MGD: MGI:109322; Kcnkl.
CC INTERPRO: IPR000099; -.
CC INTERPRO: IPR001622; -.
CC INTERPRO: IPR001779; -.
CC PRAM: PR02034; TWIK_channel; 1.
CC PRINTS: PR01096; TWIKCHANNEL.
CC DR IONIC channel; Transmembrane; Ion transport; Potassium transport;
CC KMW Glycoprotein; Phosphorylation.
CC FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 21 41 POTENTIAL.
CC FT DOMAIN 104 130 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 133 153 POTENTIAL.
CC FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 178 198 POTENTIAL.
CC FT DOMAIN 212 238 PORE-FORMING (POTENTIAL).
CC FT TRANSSEM 247 267 POTENTIAL.
CC FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
CC FT MOD_RES 19 19 PHOSPHORYLATION (BY CAM-KINASE II)
CC (POTENTIAL).
CC MOD_RES 303 303 PHOSPHORYLATION (BY CK2) (POTENTIAL).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. -) (POTENTIAL).
CC SQ SEQUENCE 336 AA; 38275 MW; A996060A18266F14 CRC64;

Query Match 94.6%; Score 1658; DB 11; Length 336;
Best Local Similarity 94.0%; Pred. No. 2.1e-137;
Matches 316; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLOSAGSSCVRLVERHRSAMCFGLVLYLVFGAVVSSVELPEYEDLLRQELRLK 60
DB 1 MLOSAGSSCVRLVERHRSAMCFGLVLYLVFGAVVSSVELPEYEDLLRQELRLK 60
QY 61 RRFLEEHCESEQLEQFLGRVLEASNYGVSVLSNAGNMIMDTSLAFRASTVLSSTGY 120
DB 61 RRFLEEHCESEQLEQFLGRVLEASNYGVSVLSNAGNMIMDTSLAFRASTVLSSTGY 120
QY 121 GHVPLSDGKAFCIITSVIGIPPTLLFLFVAVOIRIVHVRPVLFFHIRMGSKOVYA 180
DB 121 GHVPLSDGKAFCIITSVIGIPPTLLFLFVAVOIRIVHVRPVLFFHIRMGSKOVYA 180
QY 181 IVAHVLGFYVSCFFFIIPAIVFVSLDDNMNLFESFYFCFISLSTIGLDVPEGYNOK 240
DB 181 IVAHVLGFYVSCFFFIIPAIVFVSLDDNMNLFESFYFCFISLSTIGLDVPEGYNOK 240
QY 241 FRELTKIGITCYLLGLIAMLVLETFCELHEKFKRMFVKKDKEDVDHIIHEHOLS 300
DB 241 FRELTKIGITCYLLGLIAMLVLETFCELHEKFKRMFVKKDKEDVDHIIHEHOLS 300
QY 301 FSSITDQAGMKEDOKNEPFVATQSSACVDGPANH 336
DB 301 FSSITDQAGMKEDOKNEPFVATQSSACVDGPANH 336

DB 301 FSSVTEQVAGLKEKQSEPFVASQSPPEYEDGSADH 336

RESULT 4
ID 002821 PRELIMINARY; PRT; 259 AA.
AC 002821;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUN-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE DOUBLE PORE POTASSIUM CHANNEL RABCKNK1 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Orlas M., Velazquez H., Tung F., Desir G.V.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF004695; AAB61602.1; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR001779; -.
DR PRINTS: PR01096; TWIKCHANNEL.
DR PRINTS: PR01333; 2PORECHANNEL.
FT NON_TER 1 1
FT NON_TER 259 259
SQ SEQUENCE 259 AA; 29311 MW; 5546A8BD27BE79F3 CRC64;

Query Match 73.7%; Score 1292.5; DB 6; Length 259;
Best Local Similarity 95.7%; Pred. No. 9.3e-98;
Matches 247; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 1 MLOSAGSSCVRLVERHRSAMCFGLVLYLVFGAVVSSVELPEYEDLLRQELRLK 60
DB 3 MLOSAGSSCVRLVERHRSAMCFGLVLYLVFGAVVSSVELPEYEDLLRQELRLK 61
QY 61 RRFLEEHCESEQLEQFLGRVLEASNYGVSVLSNAGNMIMDTSLAFRASTVLSSTGY 120
DB 62 RRFLEEHCESEQLEQFLGRVLEASNYGVSVLSNAGNMIMDTSLAFRASTVLSSTGY 121
QY 121 GHVPLSDGKAFCIITSVIGIPPTLLFLFVAVOIRIVHVRPVLFFHIRMGSKOVYA 180
DB 122 GHVPLSDGKAFCIITSVIGIPPTLLFLFVAVOIRIVHVRPVLFFHIRMGSKOVYA 181
QY 181 IVAHVLGFYVSCFFFIIPAIVFVSLDDNMNLFESFYFCFISLSTIGLDVPEGYNOK 240
DB 182 IVAHVLGFYVSCFFFIIPAIVFVSLDDNMNLFESFYFCFISLSTIGLDVPEGYNOK 241
QY 241 FRELTKIGITCYLLGLI 258
DB 242 FRELTKIGITCYLLGLI 259

RESULT 5
ID 091257 PRELIMINARY; PRT; 313 AA.
AC 091257;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-2 (TANDEM PORE DOMAIN
DE POTASSIUM CHANNEL) (TWIK-ORIGINATED SIMILARITY SEQUENCE TOSS).
GN KNC6 OR TWIK2 OR TWIK-2 OR TOSS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=TESTIS;
RC MEDLINE=99285568; PubMed=10359073;
RA Pounney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes D.,

RA Saganich M., Rudy B., Artman M., Coetzee W.A.;
 RT Identification and cloning of TWIK-originated similarity sequence
 RL (TOS): a novel human 2-pore K⁺ channel principal subunit.";
 FEBS Lett. 450:191-196(1999).
 [2]
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-53.
 RP TISSUE-BRAIN:
 RX MEDLINE-99175162; PubMed-10075682;
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RA Mehta Y., Forsayeth J.R., Yost C.S.;
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain
 potassium channel family".
 RL J. Biol. Chem. 274:7887-7892(1999).
 RN [3]
 RP ERRATUM.
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
 RA Mehta Y., Forsayeth J.R., Yost C.S.;
 RL J. Biol. Chem. 274:24440-24440(1999).
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
 TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
 PLACENTA, PANCREAS, HEART, COLON AND SPLEEN. LOWER LEVELS DETECTED
 IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
 CC LOWEST EXPRESSION DETECTED IN BRAIN.
 CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL
 DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CHANNELS.
 DR EMBL: AF134149; AAD22980.1; -;
 DR EMBL: AF117708; AAD24000.1; -;
 DR MIM: 603939; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR001779; -;
 DR PRINTS: PR01096; TWIK1CHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;
 KW Potassium transport; Phosphorylation.
 FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 FT TRANSMM 5 25 POTENTIAL.
 FT DOMAIN 90 115 PORE-FORMING (POTENTIAL).
 FT TRANSMM 121 141 POTENTIAL.
 FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSMM 173 193 POTENTIAL.
 FT DOMAIN 199 223 PORE-FORMING (POTENTIAL).
 FT TRANSMM 236 256 POTENTIAL.
 FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 158 158 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 304 304 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 53 53 C->A: NO CHANNEL ACTIVITY.
 SQ SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;

Query Match 37.3%; Score 653.5; DB 4; Length 313;
 Best Local Similarity 45.3%; Pred. NO. 1.4e-45;
 Matches 140; Conservative 58; Mismatches 86; Indels 25; Gaps 7;

QY 24 GFLVIG----YLYVYFPAVYSSVELPYEDLLROELRKRLREHEHCLSEQLEQFL 79
 DB 4 GALLAGALAAVAAVYVLAALLVARLEGPEARLRALETLRLQOLLQSPCVAAPIADAFV 63
 QY 80 GVLEASNYGVSVLSNAGNMN----WDFTSALFFASTVLTSTGTGHTVPLSDGKAF 134
 DB 64 ERYLAAGLGRVYLANAGSANAADPAMDFASALFFASTLITTYGTYTTPITLDGKAF 123
 QY 135 IYISYIGIPFTLFLTAVALVQRTVHTRRPVLYFHIRMGFSKQOVAIVHAV-LIGFVTVS 193
 DB 124 IAFALIGVPTWLLTLTAQAORSLTLTLTHVPLSMRGMMDPRRAACWHLVALLGVVTV 183
 QY 194 CFFIIPAVSVLEDDNMFLESFYFCFISLSLTIGLDYVPGGVIQOKRELKXITCYL 253

DB 184 C-FLYPAVIAHLEAMWSFLDAFYECFISLTIGLDYVPGAPGPYRALYKVLTVYL 242
 QY 254 LGLIAMLVLEFTEFELHKKRKFMY-----KKDKEDGYHII-----EHDLS 300
 DB 243 FLGVAMVVLQTFRRVSDHLGLTLLPCCPASFNADP-DRYDILQPPESHQOLS 301
 QY 301 FSSITDQAA 309
 DB 302 ASSHTDYAS 310
 RESULT 6
 Q9J14 PRELIMINARY; PRT; 343 AA.
 AC Q9J14;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TWO PORE DOMAIN K+ CHANNEL SUBUNIT.
 GN KCNK6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/JOLA;
 RA Saridaki A., Ferraz C., Demaille J., Scherer G., Roux A.-F.;
 RT "Genomic sequencing reveals the structure of the knck6 and Map3k1
 genes and their close vicinity to the Slp1 gene on mouse chromosome
 RT 19.";
 RL Cytogenet. Cell Genet. 89:85-88(2000).
 DR EMBL: AF15142; AAF73282.1; -;
 KW Ionic channel.
 SQ SEQUENCE 343 AA; 35993 MW; 7D3672F3AA284168 CRC64;

Query Match 30.4%; Score 532.5; DB 11; Length 343;
 Best Local Similarity 38.3%; Pred. NO. 1.1e-35;
 Matches 124; Conservative 59; Mismatches 124; Indels 17; Gaps 6;

QY 26 LVLYGLTVLYFCAVYSSVELPYEDLLROELRKRLREHEHCLSEQLEQFLGRVLE 84
 DB 13 LLMHLMLMGCAVLAQLGEPARHQAQVLAELASQAHEHRAICPEALELLGAVLR 72
 QY 85 ASNYGVSVLSNAGNMNDFTSALFFASTVLTSTGTGHTVPLSDGKAFCTIYSYIGIP 144
 DB 73 AOHAGVSSLSGNSSETSNMDLPALFTASTLITTYGHTGMAPLSGKAFVYVYALGLPA 132
 QY 145 TLLFLTAVALVQRTVHTRRPVLYFHIRMGFSKQOVAIVHAVLIGFVTVSCFFIIPAVFS 204
 DB 133 SLA-LVAALRHGLLPFSRPGDWAIIRQGLAPAQAALLQAAGLGLVACVFWLPAVLVW 191
 QY 205 VLEDWMNLFESYFCFISLSLTIGLDYV--GEGYNQKRELKXITCYLILGLIAMLY 262
 DB 192 GVQGCSSLEALYFCFISLTIGLDLPAHGRGHAPAIYHNGQFALGLLGLIAMLL 251
 QY 263 VLETCFELHELKKFRKMYVKDK--DEQVHIEHDOLSFSSITDQ-----AGKE 313
 DB 252 AVEITSELPQVAMYKFRGPGSSRTDEDQDGLIGODELALSTVLPDAVPLGPTPASVSE 311
 QY 314 DQKQNEPVAITOSAC---VDGP 333
 DB 312 HQNRQPADPQATGSGATSGQDRAVGP 335
 RESULT 7
 Q9Y202 PRELIMINARY; PRT; 307 AA.
 ID Q9Y202;
 AC Q9Y202; Q9Y204; Q9Y203;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

DR INTERPRO: IPR000099; -
 DR INTERPRO: IPR001622; -
 DR PFAM: PF02034; TWIK_channel; 1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 1 10
 FT TRANSMEM 11 31
 FT TRANSMEM 92 118
 FT TRANSMEM 120 140
 FT TRANSMEM 141 172
 FT TRANSMEM 173 193
 FT TRANSMEM 199 227
 FT TRANSMEM 223 253
 FT TRANSMEM 254 307
 FT MOD_RES 3 3
 FT MOD_RES 255 255
 FT MOD_RES 274 274
 FT MOD_RES 276 276
 FT CARBOHD 83 83
 FT CONFLICT 1 3
 FT CONFLICT 2 3
 FT CONFLICT 2 3
 FT CONFLICT 84 84
 FT CONFLICT 231 232
 FT CONFLICT 293 293
 SQ SEQUENCE 307 AA; 32168 MW; 567D32AE355BA44F CRC64;

Query Match 29.6%; Score 518.5; DB 11; Length 307;
 Best Local Similarity 40.4%; Pred. No. 1.3e-34;
 Matches 116; Conservative 52; Mismatches 114; Indels 5; Gaps 4;

QY 26 LVLYGLLYLVFAGAVVSSVELPYEDLLRQELRKRRFLKEE-CLSEQLQELGRVLE 84
 DB 13 LMAHLGLAGLVVQLAEGPARHLQAOVALASFAEHKACLPPEALELLGAVLR 72
 QY 85 ASNYGVSVLSNAGNMNDFTSLFPASTVLTSTGYGHTVPLSDGKACFIYVIGIPF 144
 DB 73 AOAHGVSIGNSESTSNMPLPSALLETASILTGTGYGHMAPLSSGGKACVYAALGLPA 132
 QY 145 TLFLFLAVVQRTVHTRRPVLYFHRMGFSKQVAIVAVNLGFTVSCFFPIPAVVS 204
 DB 133 SLA-LVAALRHCLLPFSRPGMVALLRWQLAPQALLQAAAGILLVACVFMILPALVLM 191
 QY 205 VLEDWMNLFSEYFCFISLSTIGLDYVP--GEGYNOKFRELYKIGITCYLLGLTAMLY 262
 DB 192 GVGQDCLLEAIYFCGSLSTIGLDLPAHGRGLPAIYHLCQFALLGLLGLLML 251
 QY 263 VLEFCEHLELKKFRKMYVKKDK-DEDOVHIIEHDQLSFSSITDQA 308
 DB 252 AVEFSELPQVRAMVKFFGSGSRDEDDGILGOELALSTVLPA 298
 RESULT 9
 Q9NEV3 PRELIMINARY; PRT: 392 AA.
 AC Q9NEV3; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Y396B.F. PROTEIN.
 GN Y396B.F.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT Investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: AL132896; CAB60911.1; -
 SQ SEQUENCE 392 AA; 45061 MW; A14CB4FBD02E0D33 CRC64;

Query Match 24.6%; Score 430.5; DB 5; Length 392;
 Best Local Similarity 38.3%; Pred. No. 2.6e-27;
 Matches 101; Conservative 47; Mismatches 83; Indels 33; Gaps 7;

QY 41 FSSVELPYEDLLRQELRKRRFLKEE-HECLSEQLQELGRVLEASNYGVSVLSNAG 98
 DB 118 FSRIEYELKIRREAVLDYQNMQRDLIOLDIDESIDKLFNIREAALGIMDMRNLIS 177
 QY 99 NMNWDFTSLFPASTVLTSTGYGHTVPLSDGKACFIYVIGIPFTLLFNAVQRTIV 158
 DB 178 DPMWTFGQAFFAAGTILSTVGVGRVSPREYGRKFLILCVIGIPITLALSAIARM-- 235
 QY 159 HTYRFPVLYFHRMGFSKQ-----VVAIVAVNLGFTVSCFFPIPAVVS 204
 DB 236 ---REP---SHKLRGLNRLGHLFTVNIQLIHGVAFASLLEY-----FAIPAVVS 284
 QY 205 VLEDWMNLFSEYFCFISLSTIGLDYVPGEYGNOKFRELYKIGITCYLLGLTAMLYVL 264
 DB 285 SIETDMSYLDAYCFVSLTIGLDYFEPDNPQSFRLYKIGATVYLMGSLCCMMLFL 344
 QY 265 ETEFCEHLELKKFR-KMYVKKDKD 287
 DB 345 AT---LYDIPQFNLSFFVKSDDE 365

RESULT 10
 Q9JIS4 PRELIMINARY; PRT: 538 AA.
 AC Q9JIS4; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL TREK-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bang H., Kim Y., Kim D.;
 RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
 RT family.";
 RL J. Biol. Chem. 275:17412-17419(2000).
 DR EMBL: AF196965; AAF75132.1; -
 SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0A52B97E4 CRC64;

Query Match 22.6%; Score 396; DB 11; Length 538;
 Best Local Similarity 32.9%; Pred. No. 2.5e-24;
 Matches 94; Conservative 54; Mismatches 104; Indels 34; Gaps 9;

QY 25 FVLVGLIYLVGAVVSSVELPYEDLLRQELRKRRFLKEECLSEQLQELGRVLE 84
 DB 76 FVVV--VYLVVGLVFRALQEPFSSOKNTALKAELRDHICVSPQELFTLIQHMLD 133
 QY 85 ASNYGVSVLSNAGNMNWDFTSLFPASTVLTSTGYGHTVPLSDGKACFIYVIGIP 143
 DB 134 ADNAGVSPVGNSSNSHMDLSAFAFFACTVITITGYINIASGKIFCLVIAIFGIP 193
 QY 144 FTLLFLTAV-----VQRTVHTRRPVLYFHRMGFSKQVAIVAVNLGFTV 192
 DB 194 LFGPILLAGIGDGLTIFKSIARVEYFRKKQY-----SQKRIYISITL--FLA 242
 QY 193 SCFFF--IPAAVSVLEDWMNLFSEYFCFISLSTIGLDYVPGEYGNOKFRELYKIGIT 250

DB 243 GCIVETIPAVIEKYLE-GWTALESIFVVTFTTGVGSDVAGNAGINREMYKPLW 301
 QY 251 CYLLGLIAMLVLETFCE-IHELKKRKMVYKDKDEDVHIIE 295
 DB 302 FWILVGLATFAVAVLSMIGDMLRVLSK-----TKREVEGETKAHAAE 342

RESULT 11
 095069 PRELIMINARY; PRT; 426 AA.

AC 095069; 090NE3;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE
 DE POTASSIUM CHANNEL TPCK1) (TREK-1 K+ CHANNEL SUBUNIT).
 GN KCN2 OR TREK.
 OS Homo sapiens (Human).
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 RT channels.",
 RL Nat. Neurosci. 2:422-426(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
 RL Submitted (May-1997) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
 CC CHLOROFORM, HALOTHANE AND ISOFURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC EMBL, AF129399; AAD47569.1; -;
 DR EMBL, AF004711; AAD01203.1; -;
 DR MIM: 603219; -;
 DR INTERPRO: IPR000099; -;
 DR INTERPRO: IPR001622; -;
 DR PFAM: PF02034; TWIK_Channel.1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 144 170
 FT TRANSMEM 172 192
 FT DOMAIN 193 223
 FT TRANSMEM 224 244
 FT DOMAIN 253 283
 FT TRANSMEM 288 308
 FT DOMAIN 309 378
 FT DOMAIN 354 426
 FT MOD_RES 38 38
 FT MOD_RES 315 315
 FT MOD_RES 318 318
 FT MOD_RES 343 343
 FT MOD_RES 348 348
 FT MOD_RES 360 360
 FT MOD_RES 366 366
 FT MOD_RES 110 110
 FT CARBOHYD 134 134
 FT CONFLICT 2 16
 FT CONFLICT 309 311
 RLV -> DML (IN REF. 2).

FT CONFLICT 391 391 S -> N (IN REF. 2).
 FT CONFLICT 411 411 A -> T (IN REF. 2).
 SQ SEQUENCE 426 AA; 47016 MM; 2ABA2336D4009F4E CRC64;

Query Match 21.8%; Score 381.5; DB 4; Length 426;
 Best local Similarity 32.7%; Pred. No. 2.8e-23;
 Matches 91; Conservative 61; Mismatches 107; Indels 19; Gaps 9;

QY 25 FVLVGLIYVFGAVVSSVELPYEDLLROELRLKRFLEHECSQQLDEQFLGAVLE 84
 DB 66 FLVAV--VLYLIGATVVKALKEPHEISQRTTIVYQKQFTLSHSCVNSTEIDELIQIYA 123
 QY 85 ASNVGVLSNAGSN--WNMFSTALFASVNLSTGIGVHPVSDGGKACIIYSGVIGP 143
 DB 124 AINAGIIPLGNTISQISHMDLGSEFFAGVITTTIGGINSIPREGGKIFCIYALGIP 183
 QY 144 FTLLFLFVAVQRIYVHTY--RPVLYFHIMGFSKQVAVIHAVLGFVTVSCFFI--P 199
 DB 184 LFGLLAGVGDQLTITGKGIAYVEDFIKNNVSQTRIRIITII--FIIFGCVLPALP 241
 QY 200 AAVFSVLEDWMNPLESFYFCFISLTIGLDYVPEGSGYNGKFRFLXIGITCYLLGLIA 259
 DB 242 AIFKHIE--GMSALDAIFYVITLTIGFDYVAG--GSDIEYLDYXPVWFWILVGLAY 299
 QY 260 MLVLETFECLEHLE--KKFRKMVYKKDKDEDVHIIE 295
 DB 300 FAVALSMIGRLVRYISK-----TKREVEGETKAHAAE 331

RESULT 12
 088454 PRELIMINARY; PRT; 398 AA.

AC 088454;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TWIK-RELATED ARACHIDONIC ACID-STIMULATED POTASSIUM CHANNEL PROTEIN
 DE TRAAK.
 GN KCNK4 OR TRAAK.
 OS Mus musculus (Mouse).
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98292450; PubMed=9628867;
 RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
 RA Lazdunski M.;
 RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
 RT polyunsaturated fatty acids.",
 RN EMBO J. 17:3297-3308(1998).
 RP ACTIVATION.
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 RT channels.",
 RL Nat. Neurosci. 2:422-426(1999).
 CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
 CC EXTERNAL K+ CONCENTRATIONS.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ISOFORM TRAAK (SHOWN HERE)
 CC AND ISOFORM TRAAK: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
 CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
 CC TESTIS.
 CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
 CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
 CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFURANE.

-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

CC EMBL: AF056492; AAC40181.1; -

DR MGD: MGI:1298234; Kcnk4.

DR INTERPRO: IPR000099; -

DR INTERPRO: IPR001622; -

DR PRAM: PR02034; TWIK-channel.1.

DR PRINTS: PR01333; 2PORECHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing; Phosphorylation.

FT DOMAIN 1 3

FT TRANSMEM 4 24

FT DOMAIN 89 113

FT TRANSMEM 119 139

FT DOMAIN 140 171

FT TRANSMEM 172 192

FT DOMAIN 198 222

FT TRANSMEM 235 255

FT DOMAIN 256 308

FT MOD_RES 146 146

FT MOD_RES 262 262

FT MOD_RES 265 265

FT MOD_RES 284 284

FT MOD_RES 288 288

FT MOD_RES 340 340

FT MOD_RES 358 358

FT MOD_RES 360 360

FT MOD_RES 379 379

FT MOD_RES 383 383

FT MOD_RES 383 383

FT CARBOHD 81 81

FT CARBOHD 84 84

FT VARSPLIC 63 67

FT VARSPLIC 68 398

SEQUENCE 398 AA; 43051 MW; 478A834B7B7AEC92 CRC64;

Query Match 21.6%; Score 379.5; DB 11; Length 398;
Best Local Similarity 34.4%; Pred. No. 3.8e-23;
Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

QY 18 RSAMCGFLVLYLVGAVVSSVELPYEDLRKRLRLEHECLSEQQLR 77
DB 2 RSTTLALAL-VLLYVSGALVFQLEOPHEQAKMDHRCDFLDHPVSOXSIED 60

QY 78 FLGRVLEASNYGVSVLSNAGNMN-----WDFTSALFPAVTLSTGHTVPLSDG 129
DB 61 FIKLIVEALGG---ANPETSWTSSNHSNMGSAFFFSGITITITIGTGNVLTDA 116

QY 130 GKACFIISVIGIPFTLLFLTAVVORITVHTRRPVLYEH--IRMGFSKQVALVAHVL 186
DB 117 GRFLCIFALVIGIPFLGMLAGVGRDGLSSLRGIGIHIEAIFLKMHPPLGVSLAVL 175

QY 187 LGFTVSCFEFT--PAAYSVLEDDMNLESEFYFCFISLSTIGLADYVPGGVNOKEREL 244
DB 176 --FLDIGLGLVLPTEFESYME-SMSKLEAIYVITLVGDDYVPGDGTQGN-SPA 231

QY 245 YKIGITCYLLGLTAMLVLET 266
DB 232 YQPLVEMWILFLGLAVFASVLT 253

RESULT 13
Q9NRT2 PRELIMINARY: PRT; 411 AA.

AC Q9NRT2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.
GN TREK-1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C., Medhurst A.D., Murdoch P., Chapman C.G.;
RT "Cloning, localization and functional expression of the human ortholog of the TREK-1 potassium channel."
RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF171068; AAF89743.1; -
KW Ionic channel.
SEQUENCE 411 AA; 45189 MW; FDE40CAB21B42A1C CRC64;

Query Match 21.6%; Score 379.5; DB 4; Length 411;
Best Local Similarity 32.5%; Pred. No. 4e-23;
Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY 25 FLVGLVLYLVGAVVSSVELPYEDLRKRLRLEHECLSEQQLRGRVLE 84
DB 51 FLVY--VLLYVSGALVFQLEOPHEISQRTIIVIQKQFISQSGCVNSTELDELQIYA 108

QY 85 ASNYGVSVLSNAGN-WMDFTSALFPAVTLSTGHTVPLSDGKAFCTIYVIGIP 143
DB 109 AINAGIIPGNTSNQISMDLSSFFFGATVITIGFISPTGKIFCTIYVALLGP 168

QY 144 FLLEFLTAVVORITVHTR--RPVLYFHIRMGFSKQVALVAHVLGVTVSCFEFT--P 199
DB 169 LEGFLIAGVGDGLTIFGKIAKVEDTPIKMWVSOFTKIRITITII--FLIGCVFLVLP 226

QY 200 AAVEVLEDDMNLESEFYFCFISLSTIGLADYVPGGVNOKERELKIGITCYLLGLIA 259
DB 227 ALIEFHIE-GMSALDAIYVITLVITLVGDDYVAG-GSDIDIEDRYKKVWEMWILVGLAY 284

QY 260 MLVLETFCE-LHELKFRKMEFYVKKDDEQVHIE 295
DB 285 FAAVLSMGDMILRVISK-----KTEEVEGERRAAAE 316

RESULT 14
Q9NYG8 PRELIMINARY: PRT; 419 AA.

AC Q9NYG8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TANDEM PORE DOMAIN POTASSIUM CHANNEL TRAAK.
GN Kcnk4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FRONTAL LOBE;
RA Gray A.T.;
RT "Assignment of Kcnk4 encoding the human potassium channel TRAAK to chromosome 11."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF247042; AAF64062.1; -
KW Ionic channel.
SEQUENCE 419 AA; 45189 MW; E7CB8E57A35CAFDF CRC64;

Query Match 21.6%; Score 378; DB 4; Length 419;
Best Local Similarity 33.7%; Pred. No. 5.4e-23;
Matches 88; Conservative 53; Mismatches 98; Indels 22; Gaps 8;

QY 18 RSAMCGFLVLYLVGAVVSSVELPYEDLRKRLRLEHECLSEQQLR 77
DB 28 RSTTLALAL-VLLYVSGALVFQLEOPHEQAKMDHRCDFLDHPVSOXSIED 60

QY 78 FLGRVLEASNYGVSLNAGNWN--WDETSALFFASTVLSITGYGHTVPLSDGGRAC 134
 DB 87 LIKEVADALGGADPETNSTNSHSAWDGSAFFPSGIIITIIIGVNALRFDAGRLFC 146
 QY 135 IIVSVIGIPFTLFLAVVORI-----TVHYTRPVLVFIHMGFSKOVAIVHAVLL 187
 DB 147 IFALVGIPLFGLLAVGGRGLSSLRHGIGHLEA-----IFLKHVPPPLVAVLSAML- 200
 QY 188 GRYVSCFFFI--PAAVSVLEDDWNPFLSEFYCFISLSTIGLGDYVPGEGYNOKRELY 245
 DB 201 -FLILICLLFVLPTFEVFCYME-DWSKLEAIVFYVITLTFVGFCDYAGADPROD-SPAY 257
 QY 246 KIGITCYLLGLLGLAMLVLET 266
 DB 258 QPLVWFILGLAVFASVLTT 278
 RESULT 15
 P97438 PRELIMINARY; PRT; 411 AA.
 AC P97438; 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE
 POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUBUNIT).
 GN KCM2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE-BRAIN;
 RX MEDLINE=97157476; PubMed=9003761;
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
 RA Lazdunski M.,
 RT "Cloning, functional expression and brain localization of a novel
 RT unconventional outward rectifier K+ channel.";
 RL EMBO J. 15:6854-6862(1996).
 RN [2]
 RP REVISIONS.
 RC TISSUE-BRAIN;
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
 RA Lazdunski M.,
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP ACTIVATION.
 RX MEDLINE=99254548; PubMed=10321245;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.,
 RT "Inhalational anesthetics activate two-pore-domain background K+
 RT channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
 CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
 CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
 CC HIPPOCAMPUS AND CEREBELLUM.
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
 CC ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
 CC ISOFLURANE.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 DR EMBL: U73488; AAC53005.2; -
 DR MGD: MGT:109366; KCM2.
 DR INTERPRO: IPR000099; -
 DR PFM: PF02034; TWIK_channel; 1.
 DR PRINTS: PRO1333; 2PORECHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KM Glycoprotein; Phosphorylation.
 FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 17 67 POTENTIAL.
 FT TRANSMEM 129 155 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 157 177 POTENTIAL.
 FT TRANSMEM 178 207 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 208 228 POTENTIAL.
 FT TRANSMEM 238 268 PORE-FORMING (POTENTIAL).
 FT TRANSMEM 273 293 POTENTIAL.
 FT TRANSMEM 294 311 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
 FT SENSITIVITY.
 FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 300 300 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 303 303 PHOSPHORYLATION (BY CAM-KINASE II)
 FT (POTENTIAL).
 FT MOD_RES 328 328 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 333 333 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 345 345 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 FT MOD_RES 351 351 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;

Query Match 21.5%; Score 376.5; DB 11; Length 411;
 Best Local Similarity 32.5%; Pred. No. 7e-23;
 Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY 25 FIVIGVLYLVFGAVVSVSELPVEDLLRQELRKRFLFEHCLSQQLEQPLGVLVE 84
 DB 51 FLVY--VLYLIGAVKALEQPOEISQRTTIVYQKQFTQAQVACVSTEDLIQDIVA 108
 QY 85 ASNYGVSLNAGN--WMDFTSALFFASTVLSITGYGHTVPLSDGGRACIIYVIGIP 143
 DB 109 AINAGIIPLGNSNQVSHMDLGSSFFAGVYITTIIGNGNSPRREGKICIIYALLGIP 168
 QY 144 FTLLFLAVVORIVHVR--RPVLYFIHMGFSKOVAIVHAVLLGPFVTSCEFFI--P 199
 DB 169 LFGFLAVGVDQLOETITGKIAKVEDFEIKWVNSQTRIRIISTII--FILEGCVLFVALP 226
 QY 200 AAVSVLEDDWNPFLSEFYCFISLSTIGLGDYVPGEGYNOKRELYKIGITCYLLGLIA 259
 DB 227 AVIFKHIE-GKSAIDAIYFYVITLTFVGFCDYAG--GSDLEYLDYKRVWFILVGLAY 284
 QY 260 MLVYLETFCE-LHELKFRKMFYVKKDDDOVHIE 295
 DB 285 FAAYLSMIGMLRVYSK-----KKEVEGEFRANAEE 316

Search completed: February 14, 2001, 03:34:29
 Job time: 28101 sec

